

U.S. Environmental Protection Agency's Toxicogenomics Partnerships Across Government, Academia, and Industry

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Genomics, proteomics, and metabonomics technologies are transforming the science of toxicology, and concurrent advances in computing and informatics are providing management and analysis solutions for this onslaught of toxicogenomic data. The U.S. Environmental Protection Agency (U.S. EPA) has been actively developing an intramural research program in genomics, proteomics, and metabonomics through a series of strategic alliances between the Office of Research and Development (ORD) and external organizations. The National Health and Environmental Effects Research Laboratory (NHEERL), National Center for Computational Toxicology (NCCT), and National Exposure Research Laboratory (NERL) have initiated a series of integrated studies wherein genomic, proteomic, and metabonomic data are being generated from both *in vivo* and *in vitro* experiments. Cooperative agreements have been established with microarray platform vendors to provide genomics expertise. Academic partners including Michigan State University and North Carolina State University have also partnered with the U.S. EPA on these toxicogenomic studies. Data from these projects have been analyzed in collaboration with various partners, including IBM, the University of Medicine and Dentistry of New Jersey, and the University of Rochester. The U.S. EPA is also collaborating on toxicogenomic quality control, data analysis and data management issues with the Food and Drug Administration's National Center for Toxicological Research, and the National Institute of Environmental Health Sciences' National Center for Toxicogenomics. Toxicogenomics has the potential to become a powerful tool in regulatory decision-making, risk assessment, and environmental monitoring (<http://www.epa.gov/osa/genomics.htm>), and these collaborative efforts provide a foundation for fulfilling this potential.

This abstract does not necessarily reflect U.S. EPA policy.